Package ‘MEALData’

October 18, 2017

Type Package

Title Example data of MEAL package

Version 1.6.0

Description The package contains methylation, expression and SNPs data obtained from GSE53261 and TCGA. It is used in MEAL case example to show MEAL functionalities.

License Artistic-2.0

LazyData TRUE

Depends R (>= 3.2.0)

biocViews Homo_sapiens_Data, MicroarrayData

RoxygenNote 6.0.1

Encoding UTF-8

NeedsCompilation no

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R topics documented:

`betavals` *Methylation values for 62 individuals*

Description

A dataset containing the beta values of more than 450k cpgs and 62 samples.

Usage

```
betavals
```

Format

A matrix with 451448 rows and 62 columns.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52025

`BRCAexpr` *Expression data of BRCA samples*

Description

An ExpressionSet containing the expression values of 14779 features and 27 samples, the phenotypic data and the annotation. It is a subset of TCGA's breast cancer samples.

Usage

```
BRCAexpr
```

Format

An ExpressionSet

Source

https://tcga-data.nci.nih.gov/tcga/dataAccessMatrix.htm

`BRCAmeth` *Methylation data of BRCA samples*

Description

A MethylationSet containing the methylation values of 384829 features and 27 samples, the phenotypic data and the annotation. It is a subset of TCGA's breast cancer samples.

Usage

```
BRCAmeth
```

Format

A MethylationSet

Source

`https://tcga-data.nci.nih.gov/tcga/dataAccessMatrix.htm`

`eset` *Expression data for 64 samples*

Description

A dataset containing expression values for 21916 features and 64 samples, the annotation of the features and the phenotypic data of the samples.

Usage

```
eset
```

Format

An `ExpressionSet`

Source

`http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE53243`

`MEALData` *MEALData: Data package used to show functionalities of MEAL package*

Description

MEALData contains data from GEO GSE53261 adapted to show MEAL functionalities. There are four datasets in the package: betavals, pheno, eset and snps.

`mset` *Methylation data for 64 samples #' A dataset containing the beta values of more than 450k cpgs and 62 samples. A dataset containing expression values for more than 450k cpgs features and 62 samples, the annotation of the features and the phenotypic data of the samples.*

Description

Methylation data for 64 samples #' A dataset containing the beta values of more than 450k cpgs and 62 samples. A dataset containing expression values for more than 450k cpgs features and 62 samples, the annotation of the features and the phenotypic data of the samples.

Usage

```
mset
```

Format

A `MethylationSet`

Source

`http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52025`

`pheno` *Phenotype values for methylation individuals*

Description

A dataset containing phenotypic variables for the 62 samples with beta values.

Usage

```
pheno
```

Format

A data.frame with 62 rows and 2 columns.

gender gender of the donnor of the fibroblast

source cell source of the fibroblast

inv inversion 17q21.31 haplotype of the sample

Source

`http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52025`

`snps` *SNPs data for 98 samples*

Description

A dataset containing genotypes for 29909 SNPs and 98 samples and the annotation of these SNPs. All the SNPs belong to chromosome 17. Probes not measuring SNPs or with only a genotype have been filtered out.

Usage

```
snps
```

Format

A list with elements:

genotypes matrix of 29909 rows and 98 columns with the genotypes in the numeric form

map data.frame of 29909 rows and 5 columns:

- Chromosome: SNP's chromosome
- snp.name: SNP's name
- position: SNP's position
- SNP: minor and major allele
- chromosome: SNP's chromosome with string "chr"

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52442

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